

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 13, 2002, 19:38:42 : Search time 100 seconds
(without alignments)
1301.067 Million cell updates/sec

Title: US-09-758-593A-1

Perfect score: 1693

Sequence: 1 MEDSEAVQATALIEQRQA.....NGLEPNDSGRETPQVPQAQ 329

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 355320 seqs, 197730502 residues

Total number of hits satisfying chosen parameters: 710640

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framat_p2n.model -DEV=xlp
-DB=/cgn2_1/USPTO_spool/US09758593/runat_13122002_193836_16276/app_query.fasta_1.519
-LOOPEXT=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0
-MAXLEN=200000000 -USER=US09758593 -CGN_1_1_36_runat_13122002_193836_16276
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -THREADS=10 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications_NA.*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	1693	100.0	1158	10 US-09-880-192-48
2	1693	100.0	1158	10 US-09-758-593A-2
3	918	54.2	576	10 US-09-758-593A-3
4	790	46.7	569	10 US-09-758-593A-5

5	662	39.1	1889	9 US-09-974-298-182
6	606	35.8	550	10 US-09-833-381-837
7	442	26.1	253	10 US-09-758-593A-4
8	437	25.8	315	10 US-09-758-593A-9
9	332	19.6	207	10 US-09-758-593A-10
10	297	17.5	255	10 US-09-758-593A-7
11	292	17.2	275	10 US-09-758-593A-8
12	276	16.3	330	10 US-09-758-593A-6
13	249.5	14.7	4134	10 US-09-841-835-1
14	247.5	14.6	4657	10 US-09-841-835-9
15	249.5	14.6	3400	10 US-09-509-196A-1
16	246	14.5	4491	10 US-09-841-835-7
17	239.5	14.1	737	10 US-09-910-943-434
18	239.5	14.1	744	9 US-09-938-842A-805
19	235	13.9	1773	10 US-09-835-788A-7
20	232.5	13.7	1299	10 US-09-808-711-12
21	232	13.7	641	10 US-09-833-381-1141
22	225	13.3	2409	9 US-09-964-899-40
23	219	12.9	1957	10 US-09-735-368-1
24	219	12.9	2505	10 US-09-947-199-3
25	219	12.9	3025	10 US-09-947-199-1
26	217.5	12.8	5352	10 US-09-833-381-1027
27	217.5	12.8	5352	10 US-09-833-381-1028
28	214	12.6	5175	9 US-09-964-899-42
29	212.5	12.6	2505	10 US-09-947-199-9
30	212.5	12.6	3026	10 US-09-947-199-7
31	212	12.5	1599	9 US-09-938-842A-1931
32	209	12.3	1356	10 US-09-815-925-7
33	207	12.2	3000	10 US-09-728-952-29
34	205.5	12.1	2826	10 US-09-728-952-30
35	205	12.1	736	10 US-09-833-381-1150
36	200	11.8	2024	10 US-09-835-788A-3
37	198.5	11.7	800	10 US-09-833-381-839
38	198	11.7	990	10 US-09-884-870-3
39	198	11.7	1538	10 US-09-884-870-1
40	197	11.6	501	10 US-09-833-790-151
41	196.5	11.6	1740	12 US-10-044-090-570
42	195.5	11.5	948	9 US-09-938-842A-2359
43	195	11.5	747	10 US-09-908-805B-38
44	195	11.5	1353	10 US-09-896-720-1
45	194	11.5	1069	10 US-09-833-381-841

ALIGNMENTS

RESULT 1
US-09-880-192-48
; Sequence 48, Application US/09880192
; Patent No. US20020077470A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael G.
; APPLICANT: Volkmut, Wayne
; APPLICANT: Klingner, Tod M.
; APPLICANT: Azimzai, Yalda
; TITLE OF INVENTION: POLYNUCLEOTIDES ASSOCIATED WITH CARDIAC MUSCLE FUNCTION
; FILE REFERENCE: PB-0009-1 CIP
; CURRENT APPLICATION NUMBER: US/09/880,192
; CURRENT FILING DATE: 2001-06-12
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PERL Program
; SEQ ID NO 48
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020077470A1 5578191CB1
US-09-880-192-48
Alignment Scores: 3.62e-169 Length: 1158
Pred. No.: 1693.00 Matches: 329
Score: 1693.00
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-880-192-48 (1-1158)

Qy	1	MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln	20
Db	20	ATGAGGAGCTCCGAGGCGGTGACAGGGCCACACGCTCATCGAGCAGCGCTGGCACAG	79
Qy	21	GluGluGlnAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu	40
Db	80	GAGGAGGAGATGAGAAATCCGAGGAGACACACGCGCAGAGCTGCCCATGTGCTG	139
Qy	41	ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly	60
Db	140	GTGCTGGAGGATGAGACACACGCGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	199
Qy	61	GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIleAspValGlyGly	80
Db	200	CAAGAGCGCTGCCAAGACGCTCCCTGGACCTCGCGGGAGATCATCGATGTGGCGGG	259
Qy	81	IleGlnAsnLeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAla	100
Db	260	ATCCAGAACCTCATCGAGCTCGGAAGAAACGACAGCAGAAAGCGGAGCGCTTGCC	319
Qy	101	AlaSerHisGluProProGluProGluIleThrGlyProValAspGluGluThr	120
Db	320	GCCTCGCATGAGCGCCCGACAGCCCGAGGAGATCACTGGCCCTGTGGATGAGGAGCC	379
Qy	121	PheLeuLysAlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGly	140
Db	380	TTCTCTGAAAGCTCGGTGGAGGGGAAATGAAGGTCAITGAGAAATTCCTGGCTGAC	439
Qy	141	GlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGlu	160
Db	440	GGTCTGAGGATGAGAGCACCACCGGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	199
Qy	161	GlyHisMetGluIleGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180
Db	500	GGCCACATGGAATCCTGGAGAGCTTCTAGATATGGGGCCACTGTGGACTTCCAGAT	559
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLys	200
Db	560	CGGCTGGACTGCACAGCCATCTGGGCTCGCCCGGGGGCCACTTAGAGGTGGTGAA	619
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu	220
Db	620	CTTCTGCAAGCCATGGAGCAGACACCAATGTGAGGGATAAGCTGCTGAGCACCCCGCTG	679
Qy	221	HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu	240
Db	680	CACGTGGCAGTCCGACAGGGCAGGTGGAGATGTGGAGCACTTCTATCCCTGGGCTG	739
Qy	241	GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn	260
Db	740	GAAATCAATGCCAGACAGAGGAGGGGATGCTGCCCTGCATGACGCTGTAGGCTCAAC	799
Qy	261	ArgTyrLysIleLeuLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu	280
Db	800	CGCTACAAATCATCNAACTGCTCTCCATGGGGCTGACATGATGACCAAGAACCTG	859
Qy	281	AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu	300
Db	860	GCAGGAAACCCCGACGACCTGTGTGACGCTCTGCGAGGCTGATACCCGGCAGCCCTG	919
Qy	301	GluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg	320
Db	920	GAGCATCTGAGCGGGGCTGAGCATAACGGGCTGGAGGGGCTTAATGATAGTGGCGA	979
Qy	321	GluThrProGlnProValProAlaGln	329
Db	980	GAGACCCCTCAGCCTGTGCCAGCCAC	1006

RESULT 2

US-09-758-593A-2
; Sequence 2: Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 2
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 5578191CB1
US-09-758-593A-2

Alignment Scores: 3,62e-169 Length: 1158
Pred. No.: 1693.00 Matches: 329
Score: 1693.00 Conservative: 0
Percent Similarity: 100.00% Mismatches: 0
Best Local Similarity: 100.00% Indels: 0
Query Match: 100.00% Gaps: 0
DB: 10

US-09-758-593A-1 (1-329) x US-09-758-593A-2 (1-1158)

Qy	1	MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln	20
Db	20	ATGAGGAGCTCCGAGGCGGTGACAGGGCCACACGCTCATCGAGCAGCGCTGGCACAG	79
Qy	21	GluGluGlnAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu	40
Db	80	GAGGAGGAGATGAGAAATCCGAGGAGACACACGCGCAGAGCTGCCCATGTGCTG	139
Qy	41	ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly	60
Db	140	GTGCTGGAGGATGAGAGCACCACCGGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	199
Qy	61	GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIleAspValGlyGly	80
Db	200	CAAGAGCGCTGCCAAGACGCTCCCTGGACCTCGCGGGAGATCATCGATGTGGCGGG	259
Qy	81	IleGlnAsnLeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAla	100
Db	260	ATCCAGAACCTCATCGAGCTCGGAAGAAACGACAGCAGAAAGCGGAGCGCTTGGCC	319
Qy	101	AlaSerHisGluProProGluProGluIleThrGlyProValAspGluGluThr	120
Db	320	GCCTCGCATGAGCGCCCGACAGCCCGAGGAGATCACTGGCCCTGTGGATGAGGAGCC	379
Qy	121	PheLeuLysAlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGly	140
Db	380	TTCTCTGAAAGCTCGGTGGAGGGGAAATGAAGGTCAITGAGAAATTCCTGGCTGAC	439
Qy	141	GlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGlu	160
Db	440	GGTCTGAGGATGAGAGCACCACCGGGCTCAGAGTGCAGCCCTGCAGAGGTGAAGGC	499
Qy	161	GlyHisMetGluIleGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180
Db	500	GGCCACATGGAATCCTGGAGAGCTTCTAGATATGGGGCCACTGTGGACTTCCAGAT	559
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLys	200
Db	560	CGGCTGGACTGCACAGCCATCTGGGCTCGCCCGGGGGCCACTTAGAGGTGGTGAA	619
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu	220

|||||
Db 620 CTCTGCAAGACCATGGAGCAGACACCAATGTGAGGATAAAGCTGTGAGCACCCCGCTG 679
QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
Db 680 CACGTGGGAGTCCGACAGGCGAGGTGGAGATTGGAGCACTTTCTATCCCTGGGCGCTG 739
QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
Db 740 GAAATCAATGCCAGAGACAGGAGGGGATAGTCCCTGCATGAGCTGTGAGGCTCAAC 799
QY 261 ArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetThrLysAsnLeu 280
Db 800 CGCTACAAATCATCAAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 859
QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuThrGlnAlaAspThrArgHisAlaLeu 300
Db 860 GCAGGAAGACCCGACGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 919
QY 301 GluHisProGluProGluAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg 320
Db 920 GAGCATCTGAGCGGGGGCTGAGCATACGGGCTGGAGGGCCCTAATGATAGTGGCGA 979
QY 321 GluThrProGlnProValProAlaGln 329
Db 980 GAGACCCCTCAGCTGTGCCAGCCAG 1006

RESULT 3

US-09-758-593A-3

; Sequence 3, Application US/09758593A

; Patent No. US20020127636A1

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein

; FILE REFERENCE: PC-0025 CIP

; CURRENT APPLICATION NUMBER: US/09/758,593A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 3

; LENGTH: 576

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020127636A1 97211866

US-09-758-593A-3

Alignment Scores:
Pred. No.: 4,3e-88 Length: 576
Score: 918.00 Matches: 187
Percent Similarity: 98.42% Conservative: 0
Best Local Similarity: 98.42% Mismatches: 1
Query Match: 54.22% Indels: 2
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-3 (1-576)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuIleGluGlnArgLeuAlaGln 20
Db 10 ATGGAGGACTCCGAGCGGTGCAGAGGGCCACAGCGCTCATCAGCAGCGGCTGGCACAG 69
QY 21 GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu 40
Db 70 GAGGAGGAGAATGAGAAATCCGAGGAGACCGACGCCCAAGCTGCCATGAGCTGCTG 129
QY 41 ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly 60
Db 130 GTGCTGGAGAGTACAGAGCACCAGCGGCTCAGAGTGCAGCCCTCGAGAGGTGAGGGC 189
QY 61 GlnGluArgValArgLysThrSerLeuAspLeuArgArgGluIleIleAspValGlyGly 80
Db 190 CAAGAGCGGCTCCGAAAGACGCTCCCTGGACCTGCGCGGGGAGATCATCATGCTGGCGG 249

QY 81 IleGlnAsnLeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAla 100
Db 250 ATCCAGAACCTCATGAGCTGGGAGAAACCGACAGCAAGACGCGGACGCTGTGGCC 309
QY 101 AlaSerHisGluProProGluProGluGluIleThrGlyProValAspGluGluThr 120
Db 310 GCCTCGCATGAGCGCGCCCGCAGAGGAGATCCTGCGCCCTGTGATGAGGAGACC 369
QY 121 PheLeuLysAlaAlaValGluGlyLys-MetLysValIleGluLysPheLeuAlaAspG 140
Db 370 TTCTCTGAAAGCTGCGGTGGAGGGGAAACATGAAGGTCTATTGAGAGCTTCTGCTGAC 429
QY 140 VGLYSerAlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuG 160
Db 430 GGGGTGAGCCGACAGCTGCGACCACTTCGTCGGACAGCACCTGCACCGAGCTTCCCTGGA 489
QY 160 u-GlyHisMetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnA 180
Db 490 AGGGCCACATGGAATCTCTGGAGAAAGCTCTAGATAATGGGCCACTGTGGACTTCCAGG 549
QY 180 sArgLeuAspCysThrAlaMetHis 188
Db 550 ATCGGCTGAGCTGCACAGCCATGCAT 575

RESULT 4

US-09-758-593A-5/C

; Sequence 5, Application US/09758593A

; Patent No. US20020127636A1

; GENERAL INFORMATION:

; APPLICANT: Walker, Michael, G.

; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein

; FILE REFERENCE: PC-0025 CIP

; CURRENT APPLICATION NUMBER: US/09/758,593A

; CURRENT FILING DATE: 2001-06-11

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PERL Program

; SEQ ID NO 5

; LENGTH: 569

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. US20020127636A1 97211876

US-09-758-593A-5

Alignment Scores:
Pred. No.: 1,21e-74 Length: 569
Score: 790.00 Matches: 149
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 46.66% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-5 (1-569)

QY 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuValValLys 200
Db 567 CGCGTGGACTGCACGCCATGCTGGGCTGCCGGGGGCCACTTAGAGGTGTGAA 508
QY 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
Db 507 CTCTGCAAGGCATGGAGCAGACACCAATGTGAGGGATAAGCTGTGAGCACCCTG 448
QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
Db 447 CACGTGGCAGTCCGGACAGCGAGGTGGAGATTGTGAGCAGCTTTCTATCCCTGGGCGCTG 388
QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
Db 387 GAAATCAATGCCAGACAGACAGGAGGAGTACTGCTGCTGATGAGCTGTGAGGCTCAAC 328
QY 261 ArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280

```

Db 327 CGGTACAAATCATCAAACTGCTGCTCCTCATGGGCTGACATGATGACCAAGACCTG 268
QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu 300
Db 267 GCAGAAAGACCCGACGACCTGGTGCAGCTCTGGCAGGCTGATACCCGCGACGCCCTG 208
QY 301 GluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg 320
Db 207 GAGCATCTGAGCGGGGCTGAGCATAAGCGGCTGGAGGGGCTTATGATAGTGGCGCA 148
QY 321 GluThrProGlnProValProAlaGln 329
Db 147 GAGACCCCTCAGCCTGTGCGAGCCAG 121

RESULT 5
US-09-974-298-182
; Sequence 182, Application US/09974298
; Patent No. US20020156263A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Huel-Mei
; TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
; FILE REFERENCE: PA-0037 P
; CURRENT APPLICATION NUMBER: US/09/974,298
; CURRENT FILING DATE: 2001-10-04
; PRIOR APPLICATION NUMBER: 60/238,331
; PRIOR FILING DATE: 2000-05-10
; NUMBER OF SEQ ID NOS: 194
; SOFTWARE: PERL Program
; SEQ ID NO 182
; LENGTH: 1889
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 332919.4
; NAME/KEY: unsure
; LOCATION: 1882
; OTHER INFORMATION: a, t, c, g, or other
US-09-974-298-182

Alignment Scores:
Pred. No.: 1,77e-60 Length: 1889
Score: 662.00 Matches: 141
Percent Similarity: 67.92% Conservativeness: 58
Best Local Similarity: 48.12% Mismatches: 82
Query Match: 39.10% Indels: 13
DB: 9 Gaps: 4

US-09-758-593A-1 (1-329) x US-09-974-298-182 (1-1889)
QY 14 IleGluGlnArgLeuAlaGlnGluGluAsnGluLysLeuArgGlyAspThrArgGln 33
Db 182 CTGGAAGAAGATGCAATGCTTACTTTAGAGAAGCAGGAGGATCTCAAGACACTTCTAGCC 240
QY 34 -----LysLeuProMetAspLeuValLeuGluAspGluLysHisGlyAla 50
Db 241 GGAGAGTATGAGCTGCTGTTACTTTAGAGAAGCAGGAGGATCTCAAGACACTTCTAGCC 300
QY 51 GlnSerAlaAlaLeu-----GlnLysValLysGlyGlnGluArg-----Val 64
Db 301 CACCCTGTGACCTGGGGGCAACAGTGTGAAAGCGAGAAACAACAGCAGGACGAGCTC 360
QY 65 ArgLysThrSerLeuAspLeuArgGluIleAspValGlyGlyIleGlnAsnLeu 84
Db 361 AAAAGAAAAAACAACAAAGCTTGAAAAATTTAGACAGACCTTGAATAATC 420
QY 85 IleGluLeuArgLysLysGlnLysLysArgAspAlaLeuAlaAlaSerHisGlu 104
Db 421 ATTCAACTGAAGAAAGGAAAAAATACAGGAAACTTAAAGTTCCAGTTGTAAGGAA--- 477
QY 105 ProProGluProGluGluLeuThrGlyProValAspGluGluThrPheLeuLysAla 124
|||||

```

```

Db 478 -----CCAGAACCTGAAATCATTTACGGAACTGTGATGTGCTTCTGAGGCT 531
QY 125 AlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAlaAsp 144
Db 532 GCTCTGGAGAAATAAACTGCCAGTAGTAGAAAAATCTTGTCTAGACAAGAACAAATCCAGAT 591
QY 145 ThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMetGlu 164
Db 592 GTTGTGATGATATAAAGCGACGCTCTCATAGAGCATGCTTGAAGGACATTTGGCA 651
QY 165 IleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeuAspCys 184
Db 652 ATTTGTGAGAAGTTAATGGAAGCTGGAGCCAGATCGAATCCGTGATATGTTGAATCC 711
QY 185 ThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGlnSer 204
Db 712 ACAGCCATCCACTGGCGAAGCCCTGGAGAAACCTGGATGTTTAAATTTGTTGCTGAT 771
QY 205 HisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisValAlaVal 224
Db 772 AAAGAGCAAAATATTAGCGCCGAGATAAGTTGCTCAGCACAGCGCTGCATGTGGCGGTG 831
QY 225 ArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeuGluIleAsnAla 244
Db 832 AGGACTGGCCACTATGATGCGCGGAGCATCTTATCGCCTGTGAGCAGCAGCTCAACGCC 891
QY 245 ArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArgTyrLysIle 264
Db 892 AAACACAGAGAGAGATACCCCGTTGCATGTCGCGTGAGACTGAACCGCTATAAGATG 951
QY 265 IleLysLeuLeuLeuHisGlyAlaAspMetThrLysAsnLeuAlaGlyLysThr 284
Db 952 ATCCGACTCTGATTATGATGCGCGGATCTCAACATCAAGAACTGTGCTGGGAAGACG 1011

RESULT 6
US-09-833-381-837
; Sequence 837, Application US/09833381
; Patent No. US20020132090A1
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: No. US20020132090A1 Nucleic Acid and Protein Homologs
; FILE REFERENCE: 5800-119
; CURRENT APPLICATION NUMBER: US/09/833,381
; CURRENT FILING DATE: 2001-04-11
; PRIOR APPLICATION NUMBER: 09/516,448
; PRIOR FILING DATE: 2000-02-29
; NUMBER OF SEQ ID NOS: 2050
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 837
; LENGTH: 550
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-833-381-837

Alignment Scores:
Pred. No.: 2.57e-55 Length: 550
Score: 606.00 Matches: 116
Percent Similarity: 100.00% Conservativeness: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 35.79% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-833-381-837 (1-550)
QY 214 LysLeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValGluIleValGlu 233
Db 1 AAGTGTGTGACGACCCGCTGACGTCCGACAGCGGAGGAGGAGGATTGTGGAG 60
QY 234 HisPheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGlyAspThrAlaLeu 253
|||||

```


OTHER INFORMATION: Incyte ID No. US20020127636A1 700913268H1
US-09-758-593A-10

Alignment Scores:
Pred. No.: 4.42e-27 Length: 207
Score: 332.00 Matches: 62
Percent Similarity: 95.65% Conservative: 4
Best Local Similarity: 89.86% Mismatches: 3
Query Match: 19.61% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-10 (1-207)

QY 242 ILeAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg 261
Db 1 ATCAATGCCAAGACAGAGAGAGGGGAGAGTGCCTGCATGATCCGTCGAGACTCAACCGC 60
QY 262 TyrlYsilelleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAla 281
Db 61 TACAATAATCATCAACTGCTCTTGCATGGGCGACACATGATGGCTAAGAATATGGCG 120
282 GlyLysThrProThrAspLeuValGlnLeuTrpClnAlaAspThrArgHisAlaLeuGlu 301
Db 121 GGAAGACCCCTACCGACCTGGTCCAGCTGTGGCAGCAGACACCCCGCATGCCCTGGAG 180
QY 302 HisProGluProGlyAlaGluHisAsn 310
Db 181 CACCTGAACCAAGTACGAGCAGAC 207

RESULT 10
US-09-758-593A-7
; Sequence 7, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 7
; LENGTH: 255
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 700911986H1
US-09-758-593A-7

Alignment Scores:
Pred. No.: 2.8e-23 Length: 255
Score: 297.00 Matches: 65
Percent Similarity: 82.72% Conservative: 2
Best Local Similarity: 80.25% Mismatches: 14
Query Match: 17.54% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-7 (1-255)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuGluGlnArgLeuAlaGln 20
Db 12 ATGGAGGGTCCCGAGCGCTGTGCAGAGAGCCACAGAGCTCATCGACGCGCTTGCAGAG 71
QY 21 GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuLeu 40
Db 72 GAGGAGAGACTGAGAACTTCGAGAGCCACTCTCTGGAGAGACCTCCATGGACATGCTA 131
QY 41 ValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly 60
Db 132 GTGCTAGAGGACGAGAGCGCTCGGGTGCAGAGTCTGCTTTACAAAAGGTTAAGGC 191
QY 61 GlnGluArgValArgLysThrSerLeuAspLeuArgArgGluLeuLeuValGlyGly 80

Db 192 CAAGAGCGGTGCGCAAGACATCCCTGGACTTGCAGCTGAGATCATTTGACGTGGCGG 251
QY 81 Ile 81
Db 252 ATC 254
RESULT 11
US-09-758-593A-8
; Sequence 8, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 8
; LENGTH: 275
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20020127636A1 701144158H1
US-09-758-593A-8

Alignment Scores:
Pred. No.: 1.04e-22 Length: 275
Score: 292.00 Matches: 72
Percent Similarity: 82.61% Conservative: 4
Best Local Similarity: 78.26% Mismatches: 14
Query Match: 17.25% Indels: 3
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-8 (1-275)

QY 1 MetGluAspSerGluAlaValGlnArgAlaThrAlaLeuGluGlnArgLeuAlaGln 20
Db 5 ATGGAGGGTCCCGAGCGCTGTGCAGAGAGCCACAGAGCTCATCGACGCGCTTGCAGAA 64
QY 21 --GluGluGluAsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeu 40
Db 65 TGAAGAGAGAGACTGAGAACTTCGAGAGCCACTCTCTGGAGAGACCTCCATGGACATGC 124
QY 40 euValLeuGluAspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysG 60
Db 125 TAGTGCTAGAGGACGAGAGCGCT--GGGTGCAGAGTCTGCTTTACAAAAGGTTAAGG 183
QY 60 lyGlnGluArgValArgLysThrSerLeuAspLeuArgArgGluLeuLeuAspValGly 80
Db 184 GCCAAGAGCGCGTGCAGAGACATCCCTGGACTTGGACGTGGACGTGAGATCATTTGACGTGGCG 243
QY 80 lyLeGlnAsnLeuLeuGluLeuArgLysLys 90
Db 244 GGATCCAGAACCTCATAGAACTGAGGAAAAA 275

RESULT 12
US-09-758-593A-6
; Sequence 6, Application US/09758593A
; Patent No. US20020127636A1
; GENERAL INFORMATION:
; APPLICANT: Walker, Michael, G.
; TITLE OF INVENTION: Ankyrin Repeat Domain 2 Protein
; FILE REFERENCE: PC-0025 CIP
; CURRENT APPLICATION NUMBER: US/09/758,593A
; CURRENT FILING DATE: 2001-06-11
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PERL Program
; SEQ ID NO 6
; LENGTH: 330
; TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID NO. US20020127636A1 7350215H1
US-09-758-593A-6

Alignment Scores:
Pred. No.: 6.42e-21 Length: 330
Score: 276.00 Matches: 50
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.30% Indels: 0
DB: 10 Gaps: 0

US-09-758-593A-1 (1-329) x US-09-758-593A-6 (1-330)

QY 280 LeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAla 299
DB 3 CTGGCAGGAAGACCCCGACGACCTGGTGCAGCTTGGCAGGCTGATACCCGGCACGCC 62
QY 300 LeuGluHisProGluProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGly 319
DB 63 CTGGAGCATCTCGACCGCGGGCTGAGCATACGCGCTGGAGGGCGCTAATCATAGTGGG 122
QY 320 ArgGluThrProGlnProValProAlaGln 329
DB 123 CGAGAGCCCTCAGCCTGTGCCAGCCAG 152

RESULT 13

US-09-841-835-1
Sequence 1, Application US/09841835
Patent No. US20020076795A1
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/841,835
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/196,387
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4134 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO

US-09-841-835-1
Alignment Scores:
Pred. No.: 1.2e-16 Length: 4134
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
DB: 10 Gaps: 9
US-09-758-593A-1 (1-329) x US-09-841-835-1 (1-4134)
QY 40 LeuValLeuGluAspGluLysHis-----HisGlyAlaGlnSerAlaLaLeuGln 56
DB 1455 TTGACTTATGAATTTAAAGTCTATTCTTTACTACAGCAGCCAGAGACGAGCTTAGCT 1514
QY 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgGluLeuLe 76
DB 1515 AAAGTTAA-----AAACA-----CTCGCTCTGGAAATCAT 1547
QY 77 AspValGlyGlyLeuGlnAsn-----LeuLeuGluLeuArg 88
DB 1548 AATTTCAACAACCCGAGTCTCATGAAACAGCAGCTGCTGTGGCTCTCTGCAT 1607
QY 89 LysLysArgLysGln-----Lys 94
DB 1608 CCCAACGTAAACAAGTGACAGAAATGTTACTTAGAAAGGAGCAATGTTAATGAANA 1667
QY 95 LysArgAspAlaLeuAlaSerHisGluProProGluProGluProGluLeuThrGly 114
DB 1668 AATAAAGATTTCATGACTCTCCCTGCAT----- 1694
QY 115 ProValAspGluGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValLleGlu 134
DB 1695 -----GTTGCGCCGAAAGAGCCCATATGATGTCATGGAA 1730
QY 135 LysPheLeuAlaAspGlyGlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeu 154
DB 1731 GTTCTGCATAAGCATGGCCCAAGATGATGATGATGATGATGATGATGATGATGATG 1790
QY 155 HisArgAlaSerLeuGluGlyHisMetGluLeuLeuGluLysLeuAspAsnGly---- 173
DB 1791 CATAGAGCGCGCTAGCAGCGCCACCTGCAGACCTGCGGCTCTCTGCTGAGTACGGCTCT 1850
QY 173 ----- 173
DB 1851 GACCCCTCCATCATCTCTTACAAGCTTCACAGCAGCAGATGGGCAATGAAGCAGTG 1910
QY 174 -----AlaThrValAspPheGln----- 179
DB 1911 CAGCAGATTCTGAGTGAGAGTACACCTATACGTACTTCTGATGTTGATGTTATCGACTT 1970
QY 180 -----AspArgLeu 182
DB 1971 GAGGCATCTAAAGCTGGAGACTTTGAAACTGTGAAGCAACTTTGACGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
DB 2031 AATGTGAGAGACTTAGAGGGCGCGCATTCACGCCCTTCACCTCCGACGAGGCTACAAC 2090
QY 195 HisLeuGluValLysLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
DB 2091 CGCGTCTCTGTGTAGAGTACCTGTACACCGGTGCGGATGTCATGCCAAGACAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValGluLeuValGluHis 234
DB 2151 GGTGGCTTGGTGGCCCTTCATAATGCTGTTATATGGACATATCAGGTGGGTGAGCTT 2210
QY 235 PheLeuSerLeuGlyLeuGluLeuAsnAlaArgAspArgGlyAspThrAlaLeuHis 254
DB 2211 TTAGTAAGGCATGGGGCTTCTGTCTCAATGGCGGACTTATGGAAATTTACCCCTCTCCAT 2270
QY 255 AspAlaValArgLeuAsnArgTyrLysLeuLeuLeuLeuHisGlyAlaAsp 274

```

Db 2271 GAAGCACCAGTAAAGAAAGTATGAATCTGCAAGCTCTTTTAAACATGGAGCAGAT 2330
      :::::||||| :::::||||| :::::||||| :::::||||| :::::|||||
Qy 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAla 294
      ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2331 CCAACTAAAGAAAGACAGAGATGAAATACACCTTTGGATTGTTAAAGGAAGGAGACACA 2390
      ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 295 AspThrArgHisAlaLeuGlu 301
      ||| ::::: |||||
Db 2391 GATATTCAGGACTTACTGAAA 2411
      ||| ::::: |||||

RESULT 14
US-09-841-835-9
; Sequence 9, Application US/09841835
; Patent No. US20020076795A1
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/09/841,835
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/196,387
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4657 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEetical: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..2855
US-09-841-835-9
Alignment Scores:
Pred. No.: 1,41e-16 Length: 4657
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
DB: 10 Gaps: 9

US-09-758-593A-1 (1-329) x US-09-841-835-9 (1-4657)
Qy 40 LeuValLeuGluAspGlyLysHis-----HisGlyAlaGlnSerAlaAlaLeuGln 56
      ||| ||| ::::: |||||

```

```

Db 1455 TTGACTTATGAATTTAAAGTCTATTCTTTACTACAAAGCAGCCAGAGAGCAGACTTAGCT 1514
Qy 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgArgGluIleIle 76
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1515 AAAGTTAAA-----AAACA-----CTCGCTCTGGAATCATTT 1547
      ::::: ::::: :::::
Qy 77 AspValGlyGlyIleGlnAsn-----LeuIleGluLeuArg 88
      ::::: ||||| :::::
Db 1548 AATTTCAACAACCGCAGTCTCATGAAACAGCACTGCATGTGCTGTGGCTCTCTGCGAT 1607
      ::::: ||||| :::::
Qy 89 LysLysArgLysGln-----Lys 94
      ||||| |||||
Db 1608 CCAAAACGTAACAAGTGCAGAGAAATGTTTACTTAGAAAAGGACAAATGTTAATGAAAA 1667
      ::::: ||||| :::::
Qy 95 LysArgAspAlaLeuAlaAlaSerHisGluProProGluProGluGluIleThrGly 114
      ::::: ||||| :::::
Db 1668 AATAAGATTTCATGACTCCCTGCGAT----- 1694
      |||||
Qy 115 ProValaspGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIleGlu 134
      ||||| |||||
Db 1695 -----GTTGCAGCCGAAAGAGCCCATTAATGATGTCATGGAA 1730
      :::::
Qy 135 LysPheLeuAlaaspGlyGlySerAlaAspThrCysAspGlnPheArgArgThrAlaLeu 154
      ::::: |||||
Db 1731 GTTCTGCATAAGCATGGCGCAAGATGATGCACCTGGACACCTTGGTGCAGACTGCTTG 1790
      ||||| |||||
Qy 155 HisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLysLeuLeuAspAsnGly--- 173
      ||||| ||||| ||||| |||||
Db 1791 CATAGAGCCGCTTAGCAGGCCACCTGCAGACCTGGCGCTCTCTGTGAGTTACGGCTCT 1850
      ||||| |||||
Qy 173 ----- 173
Db 1851 GACCCCTCCATCTCTCTTACAAGGCTTCACAGCAGCAGATGGCAATGAAGCAGTG 1910
      :::::
Qy 174 -----AlaThrValaspPheGln----- 179
Db 1911 CAGCAGATTCTGAGTGAGAGTACACCTATACGTACTTCTGATGTTGATTATCGACTTTA 1970
      ::::: ||||| |||||
Qy 180 -----AspArgLeu 182
      :::::
Db 1971 GAGGCATCTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTTCAGCTCTCAAAATGTG 2030
      :::::
Qy 183 AspCys-----ThrAlaMethIsthrpAlaCysArgGlyGly 194
      ::::: |||||
Db 2031 AATTGTAGAGACTTAGAGGGCGCGCATTCACGCCCTTACACTTCGCAGCAGGCTACAAC 2090
      ::::: |||||
Qy 195 HisLeuGluValValLysLeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
      ::::: ||||| ||||| |||||
Db 2091 CGCGTGTCTGTTGTAGAGTACCTGCTACACCGGTCGCGATGTCATGCCAAAGACAAG 2150
      ::::: ||||| |||||
Qy 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValGluIleValGluHis 234
      ::::: ||||| |||||
Db 2151 GTTGGCTTGTGCTCCCTTCATATGCTGTTTCATATGGACACTATGAGTGGCTGAGCTT 2210
      ::::: ||||| |||||
Qy 235 PheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHis 254
      ::::: ||||| |||||
Db 2211 TTAGTAAGGCATGGGCTTCTGTCAATGTGGCGGACTTATGGAATTTTACCCCTCTCCAT 2270
      ::::: |||||
Qy 255 AspAlaValArgLeuAsnArgTyrLysIleIleLysLeuLeuLeuHisGlyValaAsp 274
      ::::: ||||| ||||| |||||
Db 2271 GAAGCAGCAGCTAAAGAAAGTATGAAATCTGCAAGTCTCTTTTAAACATGGAGCAGAT 2330
      ::::: ||||| |||||
Qy 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAla 294
      ::::: ||||| |||||
Db 2331 CCAACTAAAGAAAGACAGAGATGGAATACACCTTTGGATTGTTAAAGGAAGGAGACACA 2390
      ::::: ||||| |||||
Qy 295 AspThrArgHisAlaLeuGlu 301
      ||| ::::: |||||
Db 2391 GATATTCAGGACTTACTGAAA 2411
      ||| ::::: |||||

RESULT 15
US-09-509-196A-1
; Sequence 1, Application US/09509196A

```


Patent No. US20020037582A1
GENERAL INFORMATION:
APPLICANT: DALY, Roger J.
APPLICANT: SUTHERLAND, Robert L.
TITLE OF INVENTION: A Potential Effector for the Grb7 Family of Signalling
TITLE OF INVENTION: Proteins
FILE REFERENCE: 1871-129
CURRENT APPLICATION NUMBER: US/09/509,196A
CURRENT FILING DATE: 2000-03-23
PRIOR APPLICATION NUMBER: P09388
PRIOR FILING DATE: 1997-09-23
PRIOR APPLICATION NUMBER: PCT A098/00795
PRIOR FILING DATE: 1998-09-23
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 3400
TYPE: DNA
ORGANISM: Homo sapiens
US-09-509-196A-1

Alignment Scores:
Pred. No.: 15e-16 Length: 3400
Score: 247.50 Matches: 105
Percent Similarity: 34.38% Conservative: 49
Best Local Similarity: 23.44% Mismatches: 133
Query Match: 14.62% Indels: 161
DB: 10 Gaps: 13

US-09-758-593a-1 (1-329) x US-09-509-196A-1 (1-3400)

QY 24 AsnGluLysLeuArgGlyAspThrArgGlnLysLeuProMetAspLeuValLeuGlu 43
DB 946 TCTGAGAAGCTCATAATGAT ---GTTGTTGAA 975
QY 44 AspGluLysHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGlyGlnArg 63
DB 976 GTAGTGGTGAACATGAAGCAAGGTAATGCTCTGGATAATCTT---GGTCAGACTTCT 1032
QY 64 ValArgLysThrSer-----LeuAspLeuArgArgGluLeuLeuAspValGly 79
DB 1033 CTACACAGAGCTGCATATTGTGGTCTATCTACAAACCTGCGCCTACTCTCGAGCTATGGG 1092
QY 80 GlyIleGlnAsnLeuIleGluLeuArg-----LysLys 90
DB 1093 TGTGATCTTAACATTATATCCCTTCAGGCTTTACTGCTTTACAGATGGGAATGAAAT 1152
QY 91 ArgLysGlnLysLysArgAspAlaLeuAla---AlaSerHisGluProProGluPro 109
DB 1153 GTACAGCAACTCTCCAGAGGGTATCTCATTTAGGTAATTCAGAGCGACAGACAATG 1212
QY 110 GluGluIleThrGlyProValAspGluGluThrPheLeuLys----- 123
DB 1213 CTGGAGCTGCAAGAGCTGGAGATGCGAAACTGTAAATAAACTGTGTACTGTCAGAGT 1272
QY 124 -----AlaAlaValGlu 127
DB 1273 GTCAACTGCAGACATGAAGGCGCTCAGTCTACACCACTTCATTTCGACCTGGGTAT 1332
QY 128 GlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAlaAspThrCysAsp 147
DB 1333 AACAGAGTGTCCGTGGTAATATCTGTACAGCATGGAGCTGATGTCATGCTAAAGAT 1392
QY 148 GlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGluGlyHisMetGluIleLeuGlu 167
DB 1393 AAAGAGGCGCTTGTACCTTTGACCAATGCATGCTTCTAGGCACTATGAAAGTTCAGAA 1452
QY 168 LysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeuAspCysThrAlaMet 187
DB 1453 CTTCTTGTAAACATGGACCATGATTATGCTAGCTGATTTATGGAAATTTACACCTTTA 1512
QY 188 HisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGlnSerHisGlyAla 207
DB 188 HisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGlnSerHisGlyAla 207

DB 1513 CATGAAGCAGCAGCAAAAGAAATATGAAATTTGCAAACTTCTGCTCCAGCATGTCGA 1572
QY 208 -----Asp 208
DB 1573 GACCTTACAAAAAACAAGGATGGAATACTCCTTTGGATCTTGTAAAGATGGAGAT 1632
QY 209 ThrAsnValArgAspLysLeuLeu----- 216
DB 1633 ACAGATATTCAAGATCTGCTTAGGGGAGATGCGACTTTGCTAGATGCTGCCAAGAAGGT 1692
QY 216 ----- 216
DB 1693 TGTTTAGCCAGAGTGAAGAAGTTGCTTCTCTGATAATGTAATTTGCCGCGATACCCAA 1752
QY 217 -----SerThrProLeuHisValAlaValArgThrGlyGlnValGluIleValGlu 233
DB 1753 GGCAGACATTCAACACCTTTACATTTAGCAGCTGGTATTAATAATTTAGAAAGTTCAGAG 1812
QY 234 HisPheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGly----- 249
DB 1813 TATTGTTACACACGAGCTGATGTAATGCCAAGACAAGAGGAGCTTATTCCTTTA 1872
QY 249 ----- 249
DB 1873 CATAATGCAGCATCTTACGGGCATGTAGATGTAGCAGCTCTACTAATAAGTATAATGCA 1932
QY 250 -----AspThrAlaLeuHisAspAlaValArgLeuAsn 260
DB 1933 TCTCTCAATGCCACGGACAATGGGCTTTTCACACCTTTGCACGAGCAGCCCAAAAGGGA 1992
QY 261 ArgTyrLysIleLeuLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280
DB 1993 CGAACACAGCTTTGCTTTGTTGCTAGCCCATGGAGCTGACCCGACTCTTAAAAATCAG 2052
QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu 300
DB 2053 GAAGGACAAACACCTTTAGATTTAGTT-----TCAGCAGATGATGTCAGCGCTCTT 2103
QY 301 -----GluHisProGlu----- 304
DB 2104 CTGACAGCAGCATGCCCCCATCTGCTCTGCCCTCTTGTGTACAAAGCTCAAGTGTCAAT 2163
QY 305 -----ProGlyAlaGluHisAsnGlyLeuGluGlyProAsnAspSerGlyArg 320
DB 2164 GGTGTGAGAGCCAGGAGCCACTGCAGATGCTCTC-----TCTTCAGGTCCA 2211
QY 321 GluThrProGlnProValProAla 328
DB 2212 TCTAGCCCATCAAGCCTTTCTGCA 2235

Search completed: December 14, 2002, 01:40:35
Job time : 108 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: December 13, 2002, 19:38:42 ; Search time 71 Seconds

(without alignments)
1421.080 Million cell updates/sec

Title: US-09-758-593A-1

Perfect score: 1693

Sequence: 1 MEDSEAVQRATALIEQRQA.....NGLEGPNDSGRETQPVPVPAQ 329

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp
-Q-/cgn2_1/USPRO_pool/US09758593/runat_13122002_193835_16243/app_query.fasta_1.519
-DB=Issued_Patents_NA -QMT=fastap -SUFFIX=run1 -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09758593 -CGCN_1_1_31 @runat_13122002_193835_16243 -NCPU=6 -ICPU=3
-NO_XLPXY -NO_WMAP -LARGQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0 -DELOP=6 -DELEXT=7

Database :

- 1: Issued_Patents_NA.*
- 2: /cgn2_6/ptodata/1/ina/5A_COMB.seq.*
- 3: /cgn2_6/ptodata/1/ina/5B_COMB.seq.*
- 4: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
- 5: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
- 6: /cgn2_6/ptodata/1/ina/BACKFILES1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match	Length	ID	Description
1	667	39.4	1026	4	US-09-394-110A-3
2	249.5	14.7	4134	4	US-09-196-387-1
3	249.5	14.7	4657	4	US-09-196-387-9
4	246	14.5	4491	4	US-09-196-387-7
5	244	14.4	3498	4	US-09-350-982C-4
6	244	14.4	4512	4	US-09-350-982C-3
7	229	13.5	3454	4	US-09-082-059-1
8	227	13.4	2849	2	US-08-484-575A-5
9	227	13.4	2849	3	US-08-477-459-5
10	227	13.4	2849	3	US-08-479-869-5
11	227	13.4	2849	3	US-08-486-414-5
12	227	13.4	2849	5	PCT-US94-01826A-5

13	227	13.4	2849	5	PCT-US94-02252A-5
14	224	13.2	2200	2	US-08-462-481-3
15	224	13.2	2200	2	US-08-436-771-5
16	224	13.2	2200	2	US-08-434-998-5
17	224	13.2	2200	2	US-08-487-797-5
18	224	13.2	2200	2	US-08-701-005A-3
19	224	13.2	2200	2	US-08-479-895-3
20	224	13.2	2200	5	PCT-US95-02058-5
21	221.5	13.1	2931	3	US-08-943-956A-1
22	220	13.0	2378	4	US-08-973-005A-3
23	220	13.0	2928	2	US-08-462-481-1
24	220	13.0	2928	2	US-08-436-771-1
25	220	13.0	2928	2	US-08-436-771-3
26	220	13.0	2928	2	US-08-434-998-1
27	220	13.0	2928	2	US-08-434-998-3
28	220	13.0	2928	2	US-08-487-797-1
29	220	13.0	2928	2	US-08-487-797-3
30	220	13.0	2928	2	US-08-701-005A-1
31	220	13.0	2928	2	US-08-479-895-1
32	220	13.0	2928	5	PCT-US95-02058-1
33	220	13.0	2928	5	PCT-US95-02058-3
34	219	12.9	2200	3	US-08-943-956A-3
35	219	12.9	2505	4	US-09-291-839-3
36	219	12.9	3025	4	US-09-291-839-1
37	205.5	12.1	5235	1	US-09-031-485-35
c 38	205.5	12.1	5235	1	US-09-031-485-36
39	205.5	12.1	5235	1	US-08-847-429A-35
c 40	205.5	12.1	5235	1	US-08-847-429A-36
41	205.5	12.1	5235	3	US-09-065-474-35
c 42	205.5	12.1	5235	3	US-09-065-474-36
43	205.5	12.1	5235	4	US-09-557-034-35
c 44	205.5	12.1	5235	4	US-09-557-034-36
45	205.5	12.1	5503	1	US-09-031-485-32

ALIGNMENTS

RESULT 1
US-09-394-110A-3
; Sequence 3, Application US/09394110A
; Patent No. 6451594
; GENERAL INFORMATION:
; APPLICANT: Chien, Kenneth
; APPLICANT: Wang, Yibin
; APPLICANT: Evans, Sylvia
; TITLE OF INVENTION: No. 6451594el Recombinant Adenovirus for Tissue Specific Exp
; FILE REFERENCE: 6627-PA8045
; CURRENT APPLICATION NUMBER: US/09/394,110A
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 1026
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-394-110A-3

Alignment Scores:
Pred. No.: 1.41e-64 Length: 1026
Score: 667.00 Matches: 128
Percent Similarity: 69.85% Conservative: 55
Best Local Similarity: 48.85% Mismatches: 75
Query Match: 39.40% Indels: 4
DB: Gaps: 2

US-09-758-593A-1 (1-329) x US-09-394-110A-3 (1-1026)

Qy	49	GlyAlaGlnSerAlaAlaLeuGlnLysValLysGlyGlnGluArgValArgLysThrSer	68
Db	180	GGGGAGGAACACGGGAAACCGGAGAACCTCCGAGGAGCGAGAG---CTCAAAAGAAAAA	236
Qy	69	LeuAspLeuArgGluIlelleAspValGlyGlyIleGlnAsnLeuIleGluLeuArg	88

QY 180 -----AspArgLeu 182
Db 1971 GAGGCATTAAGCTGGAGACTTGGAAACTGTGAAGCACTTTGGCAGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
Db 2031 AATTGTAGAGACTTAGAGGGCGCGCATTCACAGCCCTTACACTTCGCACAGGCTACAAC 2090
QY 195 HisLeuGluValValLysLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
Db 2091 CGCGTGTCTGTGTAGAGTACCTGTACACACGCGGTGGCATGTCCATGCCAAAGACAAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValCulIleValGluHis 234
Db 2151 GGTGGCTTGGTCCCTTCATATGCTTCCATATGGACATATGAGGTGGCTGAGCTT 2210
QY 235 PheLeuSerLeuGlyLeuGluLeuAsnAlaArgAspArgGluGlyAspThrAlaLeuHis 254
Db 2211 TTAGTAAGGCATGGGCTTCTGCAATGTGGCGGACTTATGGAAATTTACCCCTCTCCAT 2270
QY 255 AspAlaValArgLeuAsnArgTyrLysIleIleLysLeuLeuLeuHisGlyAlaAsp 274
Db 2271 GAAGCAGCAGCTAAAGGAAGTATGAATCTGCAAGCTCTTTTAAACATGGAGCAGAT 2330
QY 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValClnLeuTrpGlnAla 294
Db 2331 CCAACTAAAGAACACAGAGATGAAATACACCTTTGGATTGGTAAAGGAAGGACACACA 2390
QY 295 AspThrArgHisAlaLeuGlu 301
Db 2391 GATATTCAGGACTTACTGAAA 2411

RESULT 3

US-09-196-387-9
; Sequence 9, Application US/09196387
; Patent No. 627613
; GENERAL INFORMATION:
; APPLICANT: de Lange, Titia
; APPLICANT: Smith, Susan
; TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
; TITLE OF INVENTION: OF USE THEREOF
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/196,387
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/095,225
; FILING DATE: June 10, 1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4657 base pairs

; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 6..2855
US-09-196-387-9
Alignment Scores:
Pred. No.: 1.83e-17 Length: 4657
Score: 249.50 Matches: 91
Percent Similarity: 35.73% Conservative: 33
Best Local Similarity: 26.22% Mismatches: 110
Query Match: 14.74% Indels: 113
Gaps: 9
US-09-758-593A-1 (1-329) x US-09-196-387-9 (1-4657)
QY 40 LeuValLeuGluAspClnLysHis-----HisGlyAlaClnSerAlaAlaLeuGln 56
Db 1455 TTGACTTATGAATTTAAAGGTCACTTTTACTACAAAGCAGCCAGAGAGCAGACTTAGCT 1514
QY 57 LysValLysGlyGlnGluArgValArgLysThrSerLeuAspLeuArgGluIleIle 76
Db 1515 AAAGTTAAA-----AAACA-----CTCGCTCTGGAATCAT 1547
QY 77 AspValGlyGlyIleGlnAsn-----LeuIleGluLeuArg 88
Db 1548 AATTTCAAAACAACCGCAGTCTCATGAAACAGCAGCTGCTGTGGCTCTCTGCAT 1607
QY 89 LysLysArgLysGln-----Lys 94
Db 1608 CCCAACGTAACCAAGTGCAGATGACAGAAATGTTACTAGAAAAGGACAAATGTTAATGAAAA 1667
QY 95 LysArgAspAlaLeuAlaAlaSerHisGluProProGluProGluThrGly 114
Db 1668 AATAAAGATTTTCATGACTCCCTGCAT----- 1694
QY 115 ProValAspGluThrPheLeuLysAlaAlaValGluGlyLysMetLysValIleGlu 134
Db 1695 -----GTTGCGCGCGAAAGCCCATATGATGTCATGGAA 1730
QY 135 LysPheLeuAlaAspGlyGlySerAlaAspThrCysAspClnPheArgArgThrAlaLeu 154
Db 1731 GTTCTGCATTAAGCATGGCCCAAGATGAATGCATGCACCCCTGGTCAGACTGCTTTG 1790
QY 155 HisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLysLeuLeuAspAsnGly--- 173
Db 1791 CATAGAGCGCGCTAGCAGCGCCACCTGCAGACCTGCCGCTCTCTGTGAGTTACGGCTCT 1850
QY 173 ----- 173
Db 1851 GACCCCTCATCATCTCTTACAAAGCTTCACAGCAGCAGATGGCAATGAAGCAGTG 1910
QY 174 -----AlaThrValAspPheGln----- 179
Db 1911 CAGCAGATTCTGAGTGAGAGTACACCTATACGTACTTCTGATGTTGATTTATCGACTCTTA 1970
QY 180 -----AspArgLeu 182
Db 1971 GAGGCATCTAAAGCTGGAGACTTGGAAACTGTGAAGCAACTTTGGCAGCTCTCAAAATGTG 2030
QY 183 AspCys-----ThrAlaMetHisTrpAlaCysArgGlyGly 194
Db 2031 AATTGTAGAGACTTAGAGGGCGCGCATTCACAGCCCTTACACTTCGCACAGGCTACAAC 2090
QY 195 HisLeuGluValValLysLeuGlnSerHisGlyAlaAspThrAsnValArgAspLys 214
Db 2091 CGCGTGTCTGTGTAGAGTACCTGTACACACGCGGTGGCATGTCCATGCCAAAGACAAAG 2150
QY 215 LeuLeuSerThrProLeuHisValAlaValArgThrGlyGlnValGluIleValGluHis 234

Db 2151 GGTGGCTTGGTCCCTTATATGCTTCTATATGACACTATGAGTGGCTGAGCTT 2210
Qy 235 PheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHis 254
Db 2211 TTAGTAAGGATGGCTTCTGTCATATGGCGGACTTATGGAATTTACCCCTCTCCAT 2270
Qy 255 AsnAlaValArgLeuAsnArgTyrLysIleIleLysLeuLeuHisGlyAlaAsp 274
Db 2271 GAAGCAGCAGCTAAGAAAGATGTAATCTGCAAGCTCTCTTTTAAACATGGAGCAGAT 2330
Qy 275 MetMetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAla 294
Db 2331 CCAACTAAAGACAGAGATGGAATACACCTTGGATTGGTAAGGAAGGAGACACA 2390
Qy 295 AspThrArgHisAlaLeuGlu 301
Db 2391 GATATTCAGGACTTACTGAAA 2411

RESULT 4

US-09-196-387-7
Sequence 7, Application US/09196387
Patent No. 6277613
GENERAL INFORMATION:
APPLICANT: de Lange, Titia
APPLICANT: Smith, Susan
TITLE OF INVENTION: A PROTEIN THAT BINDS TO TRF1 AND METHODS
TITLE OF INVENTION: OF USE THEREOF
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue, 4th Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/196,387
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/095,225
FILING DATE: June 10, 1998
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-230 CIP1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 4491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: CDS
LOCATION: 6..2027
US-09-196-387-7

Alignment Scores:
Pred. No.: 4,23e-17 Length: 4491
Score: 246.00 Matches: 82
Percent Similarity: 36.00% Conservative: 35

Best Local Similarity: 25.23% Mismatches: 102
Query Match: 14.53% Indels: 106
DB: Gaps: 7
US-09-758-593A-1 (1-329) x US-09-196-387-7 (1-4491)
Qy 64 ValArgLysThrSerLeuAspLeuArg---ArgGluIleIleAspValGlyGlyIleGln 82
Db 2295 ATACGTACTTCTGATCTTATGATTCAGCTCTTAGAGGCATCTAAAGCTGGAGACTTTGGAA 2354
Qy 83 AsnLeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSer 102
Db 2355 ACTGTGAAGCAACTTGCAGCTCTCAAAATGGAATTTAGAGAC---TTAGAGGCCGG 2411
Qy 103 HisGluProProGluProGluGluIleThrGlyProValAspGluGluThrPheLeu 122
Db 2412 CATTCACGCC---TTACAC 2429
Qy 123 LysAlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySer 142
Db 2430 TTCGACGAGGCTACAAACCGCTGTCTGTGTAGAGTACCTGTACACACCGTCCGAT 2489
Qy 143 AlaAspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
Db 2490 GTCCATGCCAAAGACAAAGGTGGCTGGTCCCTTCAATAATGCCCTGTTCATATGGACAC 2549
Qy 163 MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeu 182
Db 2550 TATGAGGTGGCTGAGCTTTTAGTAGGCGATGGGCTTCTGCTCAATGTGGCGGACTTATGG 2609
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuLeu 202
Db 2610 AAATTACCCCTCTCCATGAAGCAGCAGCTAAAGGAAGTATGAAATCTCAAGACTCCTT 2669
Qy 203 GlnSerHisGlyAla-----207
Db 2670 TTAACATCATGGAGCAGATCCAACTAAAGACAGAGATGGAATACACCTTTGGATTGG 2729
Qy 208 -----AspThrAsnValArgAspLysLeuLeu-----216
Db 2730 GTAAAGGAAGGAGACACAGATATTACGAGCTTACTGAAAGGGATGCTGCTTTGTTGGAT 2789
Qy 216 -----216
Db 2790 GCTGCCAAGAAGGCTGCTGCGCAAGAGTGCAGAAGCTGTGTACCCAGAGATATCAAC 2849
Qy 217 -----SerThrProLeuHisValAlaValArgThrGlyGln 228
Db 2850 TGCAGACACACCCAGGCGCAGAAATTCACCCCTCTGCACCTGGCAGCAGGCTATAATAC 2909
Qy 229 ValGluIleValGluHisPheLeuSerLeuGlyLeuIleAsnAlaArgAspArgGlu 248
Db 2910 CTGGAAGTAGCTGAATATCTTCTAGAGCATGGAGCTGATGTTATGTCGCCAGCAAGGT 2969
Qy 249 Gly-----249
Db 2970 GGTTTAATTCCTTTCATATGCGGCATCTTATGGGCATGTTGACATAGCGGCTTTATTG 3029
Qy 250 -----AspThrAlaLeuHisAsp 255
Db 3030 ATAAATACACACGTGTGTAAATGCAACAGATAAGTGGGGTTTACTCCCTCCATGAA 3089
Qy 256 AlaValArgLeuAsnArgTyrLysIleIleLysLeuLeuHisGlyAlaAspMet 275
Db 3090 GCAGCCAGAAAGGAAGCAGCAGCTGTGCGCCCTCTCTCTAGCGCATGGTGCAGACCCC 3149
Qy 276 MetThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAsp 295
Db 3150 ACCATGAAGAACAGGAGGCCAGCCCTCTGATCTGGCA-----ACAGCTGAC 3200
Qy 296 ThrArgHisAlaLeu 300
Db 3201 GATATCAGAGCTTTG 3215

```

RESULT 5
US-09-350-982C-4
; Sequence 4, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods Relate
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 4
; LENGTH: 3498
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: CDS
; LOCATION: (1)..(3498)
; NAME/KEY: misc.feature
; OTHER INFORMATION: Xaa is any amino acid
; NAME/KEY: misc.feature
; LOCATION: (1102)..(1102)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc.feature
; LOCATION: (2650)..(2650)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-4

Alignment Scores
Pred. No.: 4.89e-17 Length: 3498
Score: 244.00 Matches: 80
Percent Similarity: 35.26% Conservative: 30
Best Local Similarity: 25.64% Mismatches: 88
Query Match: 14.41% Indels: 114
DB: 7 Gaps: 4

US-09-758-593A-1 (1-329) x US-09-350-982C-4 (1-3498)
QY 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
Db 1597 GCAGCTGGGTATACAGAGTGCCGGTGGGAATATCTGCTACAGCATGGAGCTGATGTG 1656
QY 144 AspThrCysAspGlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMet 163
Db 1657 CATGCTAAAGATAAAGRRGSCCTTGTTACCTTTGCACAATGCATGTTCTTATGGACATTAT 1716
QY 164 GluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeuAsp 183
Db 1717 GAAGTTGCAGAACTTCTGTTAAACATGGAGCAGTAGTAAATGCTAGCTGATTATGGAAA 1776
QY 184 CysThrAlaMetHisrPlacysArgGlyHisLeuValValLysLeuGln 203
Db 1777 TTTACACCTTTACATGAACGACGCAAAAGGAAATATGAATTTGCAAACTTCGTGC 1836
QY 204 SerHisGlyAla 207
Db 1837 CAGCATGGTGCAGACCCCTACAAAAAAGAGGATGGAATACTCCTTTGGATCTTGT 1896
QY 208 -----AspThrAsnValArgAspLysLeu----- 216
Db 1897 AAAGATGGAGATACAGATATTCAAGATCTGCTTAGGGAGATGCAGCTTTGCTAGATGCT 1956
QY 216 ----- 216
Db 1957 GCCAAGAAGAGTTGTTAGCCAGATGAAGAAGTTCTCTTCCTCATATGTAATGTAATGC 2016
QY 217 -----SerThrProLeuHisValAlaValArgThrGlyGlnVal 229

```

```

Db 2017 CGGATACCAAGGCAGACATTCAACACCTTTACATTTAGCAGCTGGTTATATAATTTA 2076
QY 230 GluIleValGluHisPheLeuSerLeuGlyLeuGluIleAsnAlaArgAspArgGluGly 249
Db 2077 GAAGTTGCAGAGTATTGTTTACAAACACGAGGCTGATGTGAATGCCCAAGACAAAGGAGGA 2136
QY 249 ----- 249
Db 2137 CTATTTCCTTTACATAATGCAGCATTTACGGGCATGTAGATGTAGCAGCTCTACTAATA 2196
QY 250 -----AspThrAlaLeuHisAspAla 256
Db 2197 AAGTATAATGCATGTGTCATATGCCAGGACAAATGGCTTTCACACCTTTGCACGAAGCA 2256
QY 257 ValArgLeuAsnArgTyrLysIleLeuLysLeuLeuLeuHisGlyAlaAspMetMet 276
Db 2257 GCCCAAAGGGAGACACACAGCTTTGTGCTTTGKTCTAGCCCATGGAGCTGACCCGACT 2316
QY 277 ThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThr 296
Db 2317 CTATAAATCAGGAAGACAAACACCTTTAGATTAGTT-----TCAGCGGATGAT 2367
QY 297 ArgHisAlaLeu-----GluHisPro 303
Db 2368 GTCAGGCTCTTCTGACAGCAGCATGCCCCCATCTGCTGCCCCCTTGTTCACAAAGCCT 2427
QY 304 Glu-----ProGlyAlaGluHisAsnGlyLeuGluGlyProAsn 316
Db 2428 CAAGTCTCATGTGTGTGAGAACCCAGGAGCCACTGCAGATGCTCTC----- 2475
QY 317 AspSerGlyArgGluThrProGlnProValProAla 328
Db 2476 TCTTCAGTGCCATCTAGCCCATCAAGCCCTTTCTGCA 2511

RESULT 6
US-09-350-982C-3
; Sequence 3, Application US/09350982C
; Patent No. 6455290
; GENERAL INFORMATION:
; APPLICANT: Berthelsen, Jens
; APPLICANT: Toma, Salvatore
; APPLICANT: Isacchi, Antonella
; TITLE OF INVENTION: Tankyrase Homolog Protein(THP), Nucleic Acids, and Methods F
; TITLE OF INVENTION: Same
; FILE REFERENCE: PHRM-0043
; CURRENT APPLICATION NUMBER: US/09/350,982C
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 4512
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: PCR Primers
; NAME/KEY: misc.feature
; LOCATION: (1124)..(1124)
; OTHER INFORMATION: n is any nucleic acid
; NAME/KEY: misc.feature
; LOCATION: (2672)..(2672)
; OTHER INFORMATION: n is any nucleic acid
US-09-350-982C-3

Alignment Scores
Pred. No.: 7.09e-17 Length: 4512
Score: 244.00 Matches: 80
Percent Similarity: 35.26% Conservative: 30
Best Local Similarity: 25.64% Mismatches: 88
Query Match: 14.41% Indels: 114
DB: 4 Gaps: 7

US-09-758-593A-1 (1-329) x US-09-350-982C-3 (1-4512)

```

124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
1619 GCAGCTGGGTATAACAGAGTCCGGTGGTGAATATCTGTACAGCATGAGCTGATGTG 1678
144 AspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMet 163
1679 CATGCTAAAGATAAAGRRGSCCTTGACCTTGGACAAATGATGCTTCTTATGGACATAT 1738
164 GluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeuAsp 183
1739 GAAGTGTGAGAACTCTTGTAAACATGAGCAGCTAGTAAATAGTGTGATTTATGCAAA 1798
184 CysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGln 203
1799 TTTACACCTTTTACATGAAGCAGCAGCAAAAGGAAATATGAATTTGCAAACTTCTGCTC 1858
204 SerHisGlyAla----- 207
1859 CAGCATGTTGAGACCCCTACAAAAAAGAGGATGGAATCTCTCTTGGATCTTGT 1918
208 -----AspThrAsnValArgAspLysLeu----- 216
1919 AAAGATGAGATACAGATATTCAAGATCTGCTTAGGGGAGATGACGCTTTGCTAGATGCT 1978
216 ----- 216
1979 GCCAAGAAGAGTGTGTTAGCCAGAGTGAAGAGTGTCTCTCTGTGATAATGTAATGTC 2038
217 -----SerThrProLeuHisValAlaValArgThrGlyGlnVal 229
2039 CCGCATACCCRAAGGAGCAGCATTCACACCTTTACATTTAGCAGCTGTTATATAATTTA 2098
230 GluIleValGluHisPheLeuSerLeuGluLeuAlaAsnAlaArgAspArgGly 249
2099 GAAGTTGAGAGTATTGTTTACACAGCAGCTGATGTGAATGCCACAGACAAAGGAGGA 2158
249 ----- 249
2159 CTTATCTCTTACATAATGACCATCTTACGGGATGTAGATGTAGCAGCTCTACTAATA 2218
250 -----AspThrAlaLeuHisAspAla 256
2219 AAGTATAATGATGTGTCAATGCCAGGCAAAATGGGCTTTTACACCTTTTGCACGAAGA 2278
257 ValArgLeuAsnArgTyrLysIleLeuLysLeuLeuHisGlyAlaAspMetMet 276
2279 GCCCAAAAGGGAGCAGACAGCTTTGCTGCTGCTAGCCCTAGGAGCTGACCCGACT 2338
277 ThrLysAsnLeuAlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThr 296
2339 CTTAAAAATCAGGAAGGACAAACACCTTTAGATTAGTT-----TCACCGGATGAT 2389
297 ArgHisAlaLeu-----GluHisPro 303
2390 GTCAGGCTCTTCTGACAGCAGCATGCCCATCTGCTCTGCCCTCTTGTTTACAGCT 2449
304 Glu-----ProGlyAlaGluHisAsnGlyLeuGluGlyProAsn 316
2450 CAAGTCTCAATGGTGTGAGAGCCAGCAGCAGCAGCTGAGATGCTCTC----- 2497
317 AspSerGlyArgGluThrProGlnProValProAla 328
2498 TCTTCAGGTCCTTCTAGCCCATCAAGCCCTTCTGCA 2533

RESULT 7

US-09-082-059-1
; Sequence 1, Application US/09082059A
; Patent No. 6225086
; GENERAL INFORMATION:
; APPLICANT: Morrow, Jon S.
; APPLICANT: Devarajan, Prasad
; TITLE OF INVENTION: No. 6225086el Ankyrin Proteins and a Method for Their Identificad

FILE REFERENCE: 44574-5002-US
; CURRENT APPLICATION NUMBER: US/09/082,059A
; CURRENT FILING DATE: 1998-05-21
; EARLIER APPLICATION NUMBER: 60/047356
; EARLIER FILING DATE: 1997-05-21
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 3454

; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (131)..(3394)
; OTHER INFORMATION: DNA/protein segment- human kidney Ankyrin G119
US-09-082-059-1

Alignment Scores: 2.19e-15 Length: 3454
Pred. No.: 229.00 Matches: 57
Score: 50.00% Conservative: 32
Percent Similarity: 32.00% Mismatches: 87
Best Local Similarity: 13.53% Indels: 2
Query Match: 4 Gaps: 0
DB:

US-09-758-593A-1 (1-329) x US-09-082-059-1 (1-3454)

QY 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
Db 212 GCCTGCAAGAGATCAATCAATTAAGTAATGAACTCTCTGTAACACAGGTGATCCATC 271
QY 144 AspThrCysAspGlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHisMet 163
Db 272 CAAGCTGAACCGAGTCGGGCTTACCCCAATCATCTGCTGCTCATGGGCGCATGTA 331
QY 164 GluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAspArgLeuAsp 183
Db 332 AATATTGTATCACAACTAATGTCATCATGGAGCTTACCAACACACCAATGTGAGAGGA 391
QY 184 CysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuGln 203
Db 392 GAACAGCAGCTGCATGCGAGCTCGTCCGCCCAAGCTGAAGTTGTGCGTATCTGTA 451
QY 204 SerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisValAla 223
Db 452 CAAGCAGGAGCTCAGGTAGAGCTAAAGCTAAAGATGACCAACACCACTCCACATTTCA 511
QY 224 ValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeuGluIleAsn 243
Db 512 GCCGACTGGGAAGAGCAGCATAGTACACAGCTGTTGTCAGCAGGCGCATCTCCAAAT 571
QY 244 AlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArgTyrLys 263
Db 572 GCAGCCCAACTTCTGGGTACACCCCTTACCTTCCGCCCGAGAGGGCGCATGAGGAT 631
QY 264 IleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAlaGlyLys 283
Db 632 GTGGCGCGTCTCTTTGGATCATGGAGCTCTTTATCTATATAACAACAAGAGGATTT 691
QY 284 ThrProThrAspLeuVal--GlnLeuTrpGlnAlaAspThrArgHisAla 299
Db 692 ACTCTCTTCTATGCGCAGCAAAATATGGAAGCTTGAAGTCGCCAATCT 741

RESULT 8

US-08-484-575A-5
; Sequence 5, Application US/08484575A
; Patent No. 5925358
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran and David E. Junker
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White


```

; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,575A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq. John P
; TELEPHONE: (212)278-0450
; TELEFAX: (212)391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..1568
;
; NAME/KEY: CDS
; LOCATION: complement (1685..2848)
;
; US-08-484-575A-5
;
; Alignment Scores:
; Pred. No.: 2,74e-15 Length: 2849
; Score: 227.00 Matches: 68
; Percent Similarity: 44.44% Conservative: 48
; Best Local Similarity: 26.05% Mismatches: 99
; Query Match: 13.41% Indels: 46
; DB: 2 Gaps: 7
;
; US-09-758-593A-1 (1-329) x US-08-484-575A-5 (1-2849)
;
; QY 66 LysThrSerLeuAspLeuArgGluIlelle-----AspValGlyGlyIleGlnAsn 83
; DB 297 AAAATGCTGTTGATTTGGCGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAAA 356
;
; QY 84 LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis 103
; DB 357 CTATA-----AGATAAAGGTAATTTGGCATCAATATATCT--- 392
;
; QY 104 GluProProGluProGluIleThrGlyProValAspGluGluThrPheLeuLys 123
; DB 393 -----GTAGAGGAACACAACTCCGTTA-----ATAGAC 422
;
; QY 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
; DB 423 GCTATAAGAACCGGAATGCCAAAATAGTAGAACTATTATCAAGCAGCGGCGGAAGTT 482
;
; QY 144 AspThrCysAsp---GlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
; DB 483 AATCATGTAATTAATTAATTCCTAATCCCTTGTTAACAGCTATCAAAATAGGATCACAC 542
;
; QY 162 ----- 162
;
; DB 543 GATATAGTAAACTGCTGTTGATTAAACGGAGTTGATCTTCTATTTCGCCAGTCCCTGCC 602
;
; QY 163 -----MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp 180
; DB 603 ATAAATAAGAAAGTATAAAAACTATATAGTAGTGGTGTGAAAGTAAACACAAAAAAT 662

```

```

; QY 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValLys 200
; DB 663 GCTAAATCTAAACACTTCTTGCAATACGGGATTAAGAAATAATGACTTAGAGGTTATCAAA 722
;
; QY 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
; DB 723 ATGCTTTTGGAGTATGAGCTGATGTTAATAATAAAGATGATAACATATGTTATCTATA 782
;
; QY 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
; DB 783 CACATAGCTACTAGGAGTAATTCATATGAATCATATAAAATTACTATTAGAAAAAGTGCT 842
;
; QY 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
; DB 843 TATGCAACGCTAAAGACAATTATGTAATTCCTCCCTACATAACGGCTAAATATGGC 902
;
; QY 261 ArgTyrLysIleIleLysLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280
; DB 903 GATTATGCTGTGATTAATAATTAGTTTATAGACCACTAATAACATAAGCAATAAGTCAAC 962
;
; QY 281 AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu 300
; DB 963 AACGGTGTACACCGTTACATAACGCTATATATATATATATATATATATATATATATATAT 1013
;
; QY 301 Glu 301
; DB 1014 GAA 1016
;
; RESULT 9
; US-08-477-459-5
; Sequence 5, Application US/08477459
; Patent No. 6001369
; GENERAL INFORMATION:
; APPLICANT: Mark D. Cochran
; TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John P. White
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,459
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: White Esq. John P
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2849 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 300..1568
; FEATURE:
; NAME/KEY: CDS

```

LOCATION: complement (1685..2848)
US-08-477-459-5

Alignment Scores:

Pred. No.:	2,74e-15	Length:	2849
Score:	227.00	Matches:	68
Percent Similarity:	44.44%	Conservative:	48
Best Local Similarity:	26.05%	Mismatches:	99
Query Match:	13.41%	Indels:	46
DB:	3	Gaps:	7

US-09-758-593A-1 (1-329) x US-08-477-459-5 (1-2849)

Qy	66	LysThrSerLeuAspLeuArgGluIle	-----AspValGlyGlyLeuGlnAsn	83
Db	297	AAATGCTGTTGATGCGGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAAA	356	
Qy	84	LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis	103	
Db	357	CTTATA-----AAGAAATAAGGTAATTCATCAATATATCT---	392	
Qy	104	GluProProGluProGluGluIleThrGlyProValAspGluGluThrPheLeuLys	123	
Db	393	-----GTAGAGGAACAACACTCGTTA-----ATAGAC	422	
Qy	124	AlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGlySerAla	143	
Db	423	GCTATAAGACCGGAATGCCAAATAGTAGAATCTATTCACACCGGAGCGCAAGTT	482	
Qy	144	AspThrCysAsp---GlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHis	162	
Db	483	AATCATGTAATFACTAAATCTCTAATCCCTGTTTAAACAGCTATCAAAATAGGATCACAC	542	
Qy	162	-----	162	
Db	543	GATATAGTAAAACTGCTGTGATTAAACGGAGTTGATCTTCTATTTGCCAGTCCCTGC	602	
Qy	163	-----MetGluIleGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp	180	
Db	603	ATAATAAAGAAATGATAAAATCTATATAGATAGTGTGTAAGTAACACAAAAAT	662	
Qy	181	ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValLys	200	
Db	663	GCTAAATCTAAACCTTCTGCAATACGCGATTAAAGATAATAGCTTAGAGGTTATCAA	722	
Qy	201	LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu	220	
Db	723	ATGCTTTTGTGATGGAGCTCATGTTAATAAAGATGATAACATATGTTATCTATA	782	
Qy	221	HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu	240	
Db	783	CACATAGCTACTAGGAGTAATTCATGAAATCATAAAAATCTATTAGAAAAAGGTGCT	842	
Qy	241	GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn	260	
Db	843	TATGCAACAGCTAAAGACAAATTTATGTAATCTCCGTTACATAACCGCGCTAAATATGCG	902	
Qy	261	ArgTyrLysIleLeuLysLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu	280	
Db	903	GATTATGCTGTATTAAATGTTTAGCCATACATAAAGCAATAGCAATAGTGCAAC	962	
Qy	281	AlaGlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu	300	
Db	963	AACGGTGTACACCGGTACATAACGCTATATATAT-----AATAGATCTGCCGTA	1013	
Qy	301	Glu 301		
Db	1014	GAA 1016		

RESULT 10

US-08-479-869-5

; Sequence 5, Application US/08479869

; Patent No. 6123949

GENERAL INFORMATION:
APPLICANT: Cochran Ph.D, Mark D
TITLE OF INVENTION: Recombinant Fowlpox Virus S-FPV-043 and
TITLE OF INVENTION: Uses Thereof

NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: John P. White
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/479,869
FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/024,156
FILING DATE: 26-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: White Esq, John P
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2849 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 300..1568

FEATURE:

NAME/KEY: CDS

LOCATION: complement (1685..2848)

US-08-479-869-5

Alignment Scores:

Pred. No.:	2,74e-15	Length:	2849
Score:	227.00	Matches:	68
Percent Similarity:	44.44%	Conservative:	48
Best Local Similarity:	26.05%	Mismatches:	99
Query Match:	13.41%	Indels:	46
DB:	3	Gaps:	7

US-09-758-593A-1 (1-329) x US-08-479-869-5 (1-2849)

Qy	66	LysThrSerLeuAspLeuArgGluIle	-----AspValGlyGlyLeuGlnAsn	83
Db	297	AAATGCTGTTGATGCGGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAAA	356	
Qy	84	LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis	103	
Db	357	CTTATA-----AAGAAATAAGGTAATTCATCAATATATCT---	392	
Qy	104	GluProProGluProGluGluIleThrGlyProValAspGluGluThrPheLeuLys	123	
Db	393	-----GTAGAGGAACAACACTCGTTA-----ATAGAC	422	
Qy	124	AlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGlySerAla	143	
Db	423	GCTATAAGACCGGAATGCCAAATAGTAGAATCTATTCACACCGGAGCGCAAGTT	482	

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/01826A
FILING DATE: 28-FEB-1994

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: White Esq, John P
TELEPHONE: (212)977-9550
TELEFAX: (212)664-0525
TELEX: 422523

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2849 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
FEATURE:

NAME/KEY: CDS
LOCATION: 300..1568

FEATURE:

NAME/KEY: CDS
LOCATION: complement (1685..2848)

PCT-US94-01826A-5

Alignment Scores:
Pred. No.: 2,74e-15 Length: 2849
Score: 227.00 Matches: 68
Percent Similarity: 44.44% Conservative: 48
Best Local Similarity: 26.05% Mismatches: 99
Query Match: 13.41% Indels: 46
Db: 5 Gaps: 7

US-09-758-593A-1 (1-329) x PCT-US94-01826A-5 (1-2849)

Qy 66 LysThrSerLeuAspLeuArgGluLeuIlele-----AspValGlyLeuGlnAsn 83
Db 297 AAATGCTGTTGATGCGGTACAGAAATCTATTCGGGTGATATATCCCTAGTAGAAAA 356
Qy 84 LeuIleGluLeuArgLysLysArgLysGlnLysLysArgAspAlaLeuAlaSerHis 103
Db 357 CTATA-----AAGATAAAGGTAATTCATCAATATATCT--- 392
Qy 104 GluProProGluProGluGluLeuThrGlyProValaspGluGluThrPheLeuLys 123
Db 393 -----GTAGAGGAACAACAACCGTTA-----ATAGAC 422
Db 124 AlaAlaValGluLysMetLysValIleGluLysPheLeuAlaAspGlyLysAla 143
Db 423 GCTATAAGACCGGAATGCCAAATAGTAGAATACTATTATCAAGCAGGAGCGCAAGTT 482
Qy 144 AspThrCysAsp---GlnPheArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
Db 483 AATCATGTAAATACFAAAATTCCTAATCCCTGTTTAACAGCTATCAAAATAGGATCACAC 542
Qy 162 ----- 162
Db 543 GATATAGTAAACTGCTGTTGATTAAACGGAGTTGATCTTATTTGCCAGTCCCTGTC 602
Qy 163 -----MetGluLeuLeuGluLysLeuLeuAspAsnGlyAlaThrValAspPheGlnAsp 180
Db 603 ATAAATAAGAAATGATAAAACTATATATAGATGCTGTCGAAGTAAACACAAAAAT 662
Qy 181 ArgLeuAspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValVallys 200
Db 663 GCTAAATCTAAACCTTCTTGCAATACGCGATTAAAGATAAATGACTTAGAGGTTATCAA 722
Qy 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeu 220
Db 723 ATGCTTTTGTAGTGGAGCTGATGTTATATAAAGATGATAACATATGTTATTTCTATA 782

Qy 221 HisValAlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
Db 783 CACATAGCTACTAGGAGTAAATTCATATGAATCAATAAATTAATAAGAAAGGTGCT 842
Qy 241 GluIleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsn 260
Db 843 TATGCAACGTAAGACAAATTTATGTTATTCCTCGTTACATAACGCGGTAATATGGC 902
Qy 261 ArgTyrLysIleIleLysLeuLeuHisGlyAlaAspMetMetThrLysAsnLeu 280
Db 903 GATTATGCTTGTATTAATAGTTTGTAGACCATACTAATAACATAAGCAATAAGTGAAC 962
Qy 281 AlaGlyLysThrProThrAspLeuValGlnLeuIleThrGlnAlaAspThrArgHisAlaLeu 300
Db 963 AACGGTGTACACCGTTACATAACGCTATATATATATATATATATATATATATATATAT 1013
Qy 301 Glu 301
Db 1014 GAA 1016

RESULT 13

PCT-US94-02252A-5

Sequence 5, Application PC/TUS9402252A

GENERAL INFORMATION:

APPLICANT: Syntro Corporation, et al.

TITLE OF INVENTION: Recombinant Fowlpox Viruses and Uses Thereof

NUMBER OF SEQUENCES: 20

CORRESPONDENCE ADDRESS:

ADDRESSEE: John P. White

STREET: 30 Rockefeller Plaza

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10112

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/02252A

FILING DATE: 28-FEB-1994

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: White Esq, John P

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)977-9550

TELEFAX: (212)664-0525

TELEX: 422523

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 2849 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

FEATURE:

NAME/KEY: CDS

LOCATION: 300..1568

FEATURE:

NAME/KEY: CDS

LOCATION: complement (1685..2848)

PCT-US94-02252A-5

Alignment Scores:

Pred. No.: 2,74e-15 Length: 2849

Score: 227.00 Matches: 68

Percent Similarity: 44.44% Conservative: 48

Best Local Similarity: 26.05% Mismatches: 99

Query Match: 13.41% Indels: 46

DB: 5 Gaps: 7

US-09-758-593A-1 (1-329) x PCT-US94-02252A-5 (1-2849)

Qy 66 LysThrSerLeuAspLeuArgGluIlelle-----AspValGlyGlyileGlnAsn 83
||| |||:::||| ||| |||||| |::|::| :::|::|
Db 297 AAAATGCTGTGATTGGCGTACAGAAATATTTCGGGTGATATATCCTAGTAGAAAAA 356
||| |||:::||| ||| |||||| |::|::| :::|::|
Qy 84 LeuileLuuArgLysLysArgLysGlnLysLysArgSpAlaLeuAlaSerHis 103
||| |||:::||| ||| |||||| |::|::| :::|::|
Db 357 CTTATA-----AAGAATAAAGGTAATTGCATCAATATATCT--- 392
||| |||:::||| ||| |||||| |::|::| :::|::|
Qy 104 GluProProGluProGluGluIleThrGlyProValaspGluLuThrPheLeuLys 123
||| |||:::||| ||| |||||| |::|::| :::|::|
Db 393 -----GTAGAGGAACAACACTCCGTTA-----ATAGAC 422
||| |||:::||| ||| |||||| |::|::| :::|::|
Qy 124 AlaAlaValGluGlyLysMetLysValIleGluLysPheLeuAlaAspGlyGlySerAla 143
||| ||| |||:::||| ||| |||||| |::|::| :::|::|
Db 423 GCTATAGAACCAGGAATGCCAAAATAGTAGAACCTATTATTATCAACGACGCGCAAGTT 483
||| ||| |||:::||| ||| |||||| |::|::| :::|::|
Qy 144 AspThrCysAsp---GlnPheArgArgThrAlaLeuHisArgAlaSerLeuGluGlyHis 162
::| ::| ::|::| ||| ||| |||::| |||::| |||::|
Db 483 AATCATGTAAATACTAAAATTCCTAATCCCTTGTTAACAGCTATCAAATAAGGATCACAC 542
::| ::| ::|::| ||| ||| |||::| |||::| |||::|
Qy 162 ----- 162
Db 543 GATATAGTAAACTGCTGTTGATTACCGGAGTTGATACTTCTATTTTGCCAGTCCCCCTGC 602
Qy 163 ----MetGluIleLeuGluLysLeuLeuAspAsnGlyAlaThrValaspPheGlnAsp 180
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 603 ATAAATAAGAAATGATAAAACTATATTAGATAGTGGTGAAAGTAAACACAAAAAAT 662
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 181 ArgLeuAspCysThrAlaMetHistrpAlaCysArgGlyGlyHisLeuGluValLys 200
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 663 GCTAAATCTAAACTTCTTCGCATTACGCGATTAAAGTAATGACTTAGAGGTTATCAAA 722
Qy 201 LeuLeuGlnSerHisGlyAlaAspThrAsnValargAspLysLeuLeuSerThrProLeu 220
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 723 ATGCTTTTTGAGTATGAGGAGTAACTCATATGAATCAATAAAAGATGATAACATATGTTATTCTATA 782
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Qy 221 HisValAlaValargThrGlyGlnValGluIleValGluHisPheLeuSerLeuGlyLeu 240
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 783 CATAGTCTACTAGGAGTAATTCATATGAATCAATAAAATTAATAAGAAAAAGTGCT 842
Qy 241 GluIleAsnAlaArgaspArgGluGlyAspThrAlaLeuHisAspAlaValargLeuAsn 260
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 843 TATGCAACCGTAAAGACAATATGTTATTTCTCGTTACATAACGCGGCTAAATATGGC 902
Qy 261 ArgTyrlsylelleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysasnLeu 280
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 903 GATTATGCTTGTATTAATAGTTTATAGACCATACTAATAACATAAGCAATAAGTGCAAC 962
Qy 281 AlaGlyLysThrProThrAspleuValGlnLeuTrpGlnAlaAspThrArgHisAlaLeu 300
|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 963 AACGGGTTCACCGGTACATAACGCTACTATATAT-----AATAGATCTGCCGTA 1013
Qy 301 Glu 301
|||
Db 1014 GAA 1016

RESULT 14
US-08-462-481-3
; Sequence 3, Application US/08462481
; Patent No. 5840577
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: Hassel, Bret A.
; APPLICANT: Zhou, Aimin
; TITLE OF INVENTION: Animal 2-5A- Dependent RNases and
; TITLE OF INVENTION: Encoding Sequence therefor
; Patent No. 5840577
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:

```
Db 542 ACGGCTTTTCATGGAAGCTGCTGAGCGTGGTAACGCTGAAGCCTTAAGATTCCTTTTTCCT 601
Qy 149 -----PheArgArg----- 151
Db 602 AAGGAGGCCAATGTGAATTTGGAGCAGCAGACAGCAAGCAAGGACAAAGCGGATTGAAGCAA 661
Qy 152 -----ThrAlaLeuHisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLys 168
Db 662 GGAGCGGCCACAGCTCTCATGAGCGCTGCTGAGAGGGCCACCTGGAAGTCTTGAGAAATT 721
Qy 169 LeuLeu----AspAsnGlyAlaThrValAspPheGlnAspArg-----Leu 182
Db 722 CTCCTCAATGACATGAAGGCAGAGTCGATGCTCGGGACAACATGGGCAGAAATGCCCTG 781
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuLeu 202
Db 782 ATCCCTACTCTGCTGAATGAGTGTGAAATGTGGAG---GAGATTACTTCAATCCTG 838
Qy 203 GlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisVal 222
Db 839 ATTCAGCAGCGGGCTGATGTTAACTGAGAGGAGAGGAGGAAACACCCCTCATCGCA 898
Qy 223 AlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeu---GlyLeuGlu 241
Db 899 GCAGTGGAGAGGAACACACAGCGCTGTGTGCAGATGCTCTGAGTCGGGAGGCATAAAC 958
Qy 242 IleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg 261
Db 959 ATGATGATCCAGGATTAACGTCGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1018
Qy 262 TyrIleIleLeuLeuLeuLeuHisGlyAlaAspMetMetMetLysAsnLeuAla 281
Db 1019 AAGGAAATGTCACGCTCTCTTCTTAAAGGAGGAGCTGATAAGTGT----- 1063
Qy 282 GlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHis 298
Db 1064 -----GACGATCTTGT-----TGGATAGCCAGGAGGAATCAT 1096

RESULT 15
US-08-436-771-5
; Sequence 5, Application US/08436771
; Patent No. 5861300
; GENERAL INFORMATION:
; APPLICANT: Silverman, Robert H.
; APPLICANT: SenGupta, Dibyendu N.
; TITLE OF INVENTION: Antiviral Transgenic Plants, Vectors,
; TITLE OF INVENTION: Cells and Methods
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ruden, Barnett, McClosky, Smith, Schuster &
; ADDRESSEE: Russell
; STREET: 200 E. Broward Boulevard
; CITY: Fort Lauderdale
; STATE: Florida
; COUNTRY: USA
; ZIP: 33301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,771
; FILING DATE:
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/198,973
; FILING DATE: 18-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Manso, Peter J.
; REGISTRATION NUMBER: 32,264
; REFERENCE/DOCKET NUMBER: CUI1363-16
```

```
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 305/527/2498
; TELEFAX: 305/764/4996
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2200 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 164..2200
US-08-436-771-5

Alignment Scores:
Pred. No.: 4,04e-15 Length: 2200
Score: 224.00 Matches: 89
Percent Similarity: 41.01% Conservativity: 41
Best Local Similarity: 28.08% Mismatches: 101
Query Match: 13.23% Indels: 86
DB: 2 Gaps: 13

US-09-758-593A-1 (1-329) x US-08-436-771-5 (1-2200)
Qy 41 ValLeuGluAspGluLysHisHisGlyAlaGlnSerAlaAlaLeuGlnLysValLysGly 60
Db 227 GTTGTGGAAGATGAT-----TCTTGTGTCATCAAGCTGTTTCAGAAAG 268
Qy 61 GlnGluArgValArgLysThrSerLeuAspLeuArgGluIleLeuAspValGlyGly 80
Db 269 GGAGATGTTGTCAAGGCTC-----CAGCAATTTGTAGAAAAAGGGGCT 310
Qy 81 IleGlnAsnLeuIleGlu-----LeuArgLysLysArgLysGln 93
Db 311 GATGCCAATGCTGTGAAGACACACCTGGGGCTGGACACCTTTGCACACCGCAGTGCAGCT 370
Qy 94 LysLysArgAspAla-----LeuAlaAlaSerHisGluProProGluProGluGlu 111
Db 371 GGACGGGTAGACATTTGTAACCTCTCTGCTGTAGTCATGCTGTGACCTCATCGGAGGAAG 430
Qy 112 IleThrGlyProValAspGluThrPheLeuLysAlaAlaValGluGlyLysMetLys 131
Db 431 AAGAAATGGGGCCACC-----CCCTTCATCATTTGCTGGGATCCAGGGAGATGTGAAA 481
Qy 132 ValIleGluLysPheLeuAlaAspGlyGlySerAlaAspThrCysAspGln----- 148
Db 482 CTGCTCGAGATTCCTCTCTTTGTTGTCACAGCTCAATGAGTGTGACGAGACGAGGATTC 541
Qy 148 -----LeuArgLysLysArgLysGln 148
Db 542 ACGGCTTTCATGAAGCTGCTGAGCGTGGTAACGCTGAAGCCTTAAGATTCCTTTTTCCT 601
Qy 149 -----PheArgArg----- 151
Db 602 AAGGAGGCCAATGTCAATTTTCGACGACAGACAAAGCAAGGACAAAGCGGATTGAAGCAA 661
Qy 152 -----ThrAlaLeuHisArgAlaSerLeuGluGlyHisMetGluIleLeuGluLys 168
Db 662 GGAGCGGCCACAGCTCTCATGAGCGCTGCTGAGAGGGCCACCTGGAAGTCTTGAGAAATT 721
Qy 169 LeuLeu----AspAsnGlyAlaThrValAspPheGlnAspArg-----Leu 182
Db 722 CTCCTCAATGACATGAAGGCAGAGTCGATGCTCGGGACAACATGGGCAGAAATGCCCTG 781
Qy 183 AspCysThrAlaMetHisTrpAlaCysArgGlyGlyHisLeuGluValValLysLeuLeu 202
Db 782 ATCCCTACTCTGCTGAATGAGTGTGAAATGTGGAG---GAGATTACTTCAATCCTG 838
Qy 203 GlnSerHisGlyAlaAspThrAsnValArgAspLysLeuLeuSerThrProLeuHisVal 222
Db 839 ATTCAGCAGCGGGCTGATGTTAACTGAGAGGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 898
```

Qy 223 AlaValArgThrGlyGlnValGluIleValGluHisPheLeuSerLeu---GlyLeuGlu 241
||||| :|||::: ||||| ||:::
Db 899 GCAGTGGAGAGGAGCACACAGGCTTGGTCAGATGCTCCTCAGTCGGGAGGCATAAAC 958
Qy 242 IleAsnAlaArgAspArgGluGlyAspThrAlaLeuHisAspAlaValArgLeuAsnArg 261
||||:||||| ||||| ||||| ||||| |||||
Db 959 ATAGATGCCAGGGATAACGAGGGCAAGACAGCTCTGCTAATTGCTTTGATAAACAACTG 1018
Qy 262 TyrLysIleIleLysLeuLeuLeuHisGlyAlaAspMetMetThrLysAsnLeuAla 281
:||||:||||| ||||| ||||| ||||| |||||
Db 1019 AAGGAATTGTCAGTTGCTTCTGAAAAGGAGCTGATAGTGT----- 1063
Qy 282 GlyLysThrProThrAspLeuValGlnLeuTrpGlnAlaAspThrArgHis 298
||||| ||||| ||||| ||||| |||||
Db 1064 -----GACGATCTTGT-----TGGATAGCCAGGAGGAATCAT 1096

Search completed: December 14, 2002, 01:37:25
Job time : 87 secs

THIS PAGE BLANK (USPTO)